

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

## (i) APPLICANTS:

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(C) CITY: Hoersholm  
(D) COUNTRY: Denmark  
(E) POSTAL CODE (ZIP): DK-2970

(ii) TITLE OF INVENTION: Artificial promoter libraries for selected organisms and promoters derived from such libraries

(iii) NUMBER OF SEQUENCES: 58

## (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

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## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE IN THE US PTO: February 19, 1999  
(C) ATTORNEY DOCKET NO.: 55411.000002

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## (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: DK 886/96
- (B) FILING DATE: 23-AUG-1996
- (C) PCT APPLICATION NUMBER: PCT/DK97/00342
- (D) FILING DATE: August 25, 1997

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

## (ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:26..82
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/evidence= EXPERIMENTAL  
/standard\_name= "Artificial promoter library"  
/note= "A degenerated sequence specifying a mixture of  
artificial promoters covering a wide range of expression in  
small steps in L. lactis"

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION:31..45
- (D) OTHER INFORMATION:/standard\_name= "Consensus  
sequence"

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION:60..69
- (D) OTHER INFORMATION:/standard\_name= "Consensus  
sequence"

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## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION:74..82

(D) OTHER INFORMATION:/standard\_name= "Consensus sequence"

## (ix) FEATURE:

(A) NAME/KEY: -35\_signal

(B) LOCATION:40..45

(D) OTHER INFORMATION:/standard\_name= "-35 box"

## (ix) FEATURE:

(A) NAME/KEY: -10\_signal

(B) LOCATION:63..68

(D) OTHER INFORMATION:/standard\_name= "Pribnow box"

## (ix) FEATURE:

(A) NAME/KEY: misc\_recomb

(B) LOCATION:3..25

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION:/evidence= EXPERIMENTAL

/standard\_name= "Multiple cloning site"

/label= MCS

/note= "A sequence specifying recognition sites for the restriction endonucleases: NlaIV, BstYI, BamHI, AlwI, MboI, DpnI, AflII, MseI, SspI, NsiI."

## (ix) FEATURE:

(A) NAME/KEY: misc\_recomb

(B) LOCATION:74..98

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION:/evidence= EXPERIMENTAL

/standard\_name= "Multiple cloning site"

/label= MCS

/note= "A sequence specifying recognition sites for the restriction endonucleases: ScaI, RsaI, HpaI, HincII, MseI, SfcI, PstI, Fnu4HI, BbvI, PvuII, NspBI, AluI, EcoRI."

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CGGGATCCTT AAGAATATTA TGCATNNNNN AGTTTATTCT TGACANNNNN  
 NNNNNNNNT 60

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GGTATAATAN NANAGTACTG TTAAGTGCAG CTGAATTCGG  
100

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:23..95
- (D) OTHER INFORMATION:/standard\_name= "Artificial promoter library"  
/note= "A degenerated sequence specifying a mixture of artificial temperature regulated promoters covering a wide range of expression in small steps in L. lactis"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION:23..49
- (D) OTHER INFORMATION:/standard\_name= "Sequence providing temperature regulation to promoters"  
/note= "This sequence comprising two inverted repeats separated by a short spacer provides temperature (heat shock) regulation to promoters in Gram-positive bacteria"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION:50..60
- (D) OTHER INFORMATION:/standard\_name= "Consensus sequence"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION:75..84

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(D) OTHER INFORMATION:/standard\_name= "Consensus sequence"

(ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION:89..95

(D) OTHER INFORMATION:/standard\_name= "Consensus sequence"

(ix) FEATURE:

(A) NAME/KEY: -35\_signal

(B) LOCATION:55..60

(D) OTHER INFORMATION:/standard\_name= "-35 box"

(ix) FEATURE:

(A) NAME/KEY: -10\_signal

(B) LOCATION:78..83

(D) OTHER INFORMATION:/standard\_name= "Pribnow box"

(ix) FEATURE:

(A) NAME/KEY: misc\_recomb

(B) LOCATION:3..22

(D) OTHER INFORMATION:/standard\_name= "Multiple cloning site"

/label= MCS

/note= "A sequence specifying recognition sites for the restriction endonucleases: NlaIV, BstYI, BamHI, AlwI, MboI, DpnI, HindIII, AluI, MseI (2 sites), SspI, AseI."

(ix) FEATURE:

(A) NAME/KEY: misc\_recomb

(B) LOCATION:89..111

(D) OTHER INFORMATION:/standard\_name= "Multiple cloning site"

/label= MCS

/note= "A sequence specifying recognition sites for the restriction endonucleases: ScaI, RsaI, SfcI, PstI, Fnu4HI, BbvI, PvuII, NspBII, AluI, XbaI, MaeI, EcoRI, ApoI."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CGGGATCCAA GCTTAATATT AATTAGCACT CNNNNNNNNN GAGTGCTAAT  
TTTTTTGACA 60

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NNNNNNNNNN NNNNTGGTAT AATANNANAG TACTGCAGCT GTCTAGAATT  
CGG 113

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: protein\_bind
- (B) LOCATION:10..16
- (D) OTHER INFORMATION:/function= "Activating promoters in *S. cerevisiae*"  
/bound\_moiety= "GCN4 protein"  
/standard\_name= "Upstream activating sequence"  
/label= UAS\_GCIN4p  
/note= "A DNA sequence that specifies a binding site for the GCN4 protein, which activates the transcription of genes involved in aminoacid synthesis in *S. cerevisiae*."

(ix) FEATURE:

- (A) NAME/KEY: TATA\_signal
- (B) LOCATION:67..72
- (D) OTHER INFORMATION:/standard\_name= "TATA box"

(ix) FEATURE:

- (A) NAME/KEY: misc\_signal
- (B) LOCATION:122..144
- (D) OTHER INFORMATION:/function= "Transcription initiation"  
/standard\_name= "TI box"

(ix) FEATURE:

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- (A) NAME/KEY: protein\_bind  
 (B) LOCATION:122..144  
 (D) OTHER INFORMATION:/bound\_moiety= "Arginine repressor"  
 /standard\_name= "arginine repressor binding site"  
 /label= argR

(ix) FEATURE:

- (A) NAME/KEY: misc\_RNA  
 (B) LOCATION:145..192  
 (D) OTHER INFORMATION:/function= "Spacer"  
 /standard\_name= "Part of native sequence for ARG8  
 gene incl. first codon"

(ix) FEATURE:

- (A) NAME/KEY: misc\_recomb  
 (B) LOCATION:3..8  
 (D) OTHER INFORMATION:/standard\_name= "Recognition site  
 for restriction endonuclease EcoRI"  
 /label= EcoRI\_site

(ix) FEATURE:

- (A) NAME/KEY: misc\_recomb  
 (B) LOCATION:192..197  
 (D) OTHER INFORMATION:/standard\_name= "Recognition site  
 for restriction endonuclease BamHI"  
 /label= BamHI\_site

(ix) FEATURE:

- (A) NAME/KEY: promoter  
 (B) LOCATION:10..192  
 (D) OTHER INFORMATION:/standard\_name= "Artificial  
 promoter library"  
 /note= "A degenerated sequence specifying a mixture of  
 artificial promoters covering a wide range of expression in  
 small steps in *S. cerevisiae*"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CAGAATTCGT GACTCANNNN NNNNNNNNNN NNNNNNNNNN  
 NNNNNNNNNN NNNNNNNNNN 60

NNNNNNNNNN NNNNNNTATA AANNNNNNNN NNNNNNNNNN  
 NNNNNNNNNN NNNNNNNNNN 120

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NCTCTTAAGT GCAAGTGA CT GCGAACATTT TTTTCGTTTG TTAGAATAAT  
TCAAGAATCG 180

CTACCAATCA TGGATCCCCG

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(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Pseudomonas putida*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 1..45
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL  
/standard\_name= "Artificial promoter library"  
/note= "A degenerated sequence specifying a mixture of  
artificial promoters covering a wide range of expression in small  
steps *Pseudomonas putida*"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

NNNNNNNNTT GRNNNNNNNN NNNNNNNNNN NTATRATNNN NNNNN  
45

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..60

(D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CATACCGGAG TTTATTCTTG ACAGTTCCAC CTCGGGTTGA TATAATATCT  
CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..60

(D) OTHER INFORMATION: /standard\_name= "Constitutional

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promoter"  
/label= Cp10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CATGGCTTAG TTTATTCTTG ACAGGGTAGT ATCACTGTGA TATAATAGGA  
CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..59
- (D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CATAAGTGAG TTTATTCTTG ACCCGGACGC CCCCTTTGA TATAATAAGT  
AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..60

(D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CATATACAAG TTTATTCTTG AACTAGTCG GCCAAAATGA TATAATACCT  
GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

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(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard\_name= "Constitutional  
promoter"  
/label= Cp13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CATGCTTTAC TTTATTCTTG ACAAACCAC CAGCTTTTGG TATAATACGT  
GAGAACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:4..60
- (D) OTHER INFORMATION:/standard\_name= "Constitutional  
promoter"  
/label= Cp14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

CATGACGGAG TTTATTCTTG ACACAGGTAT GGAATTATGA TATAATAAAA  
CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 11:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

## (ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp15

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CATTACNTAG TTNATTCTTG ACAGAATTAC GATTCGCTGG TATAATATAT  
CAGTACTGTT 60

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

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## (ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..58

(D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp16

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CATTGTGTAG TTTATTCTTG ACAGCTATGA GTCAATTTGG TATAATAACA  
GTACTCAG 58

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

## (ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..59

(D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp17

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CATTCTGGAG TTTATTCTTG ACCGCTCAGT ATGCAGTGGT ATAATAGTAC  
AGTACTGTT 59

## (2) INFORMATION FOR SEQ ID NO: 14:

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cont.

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

## (ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..58
- (D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp18

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

CATTTTGCAG TTTATTCTTG ACATTGTGTG CTTCGGGTGT ATAATACTAA  
GTACTGTT 58

## (2) INFORMATION FOR SEQ ID NO: 15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

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## (ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..58

(D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp19

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CATCGCTTAG TTTTCTTGA CAGGAGGGAT CCGGGTTGAT ATAATAGTTA  
GTACTGTT 58

## (2) INFORMATION FOR SEQ ID NO: 16:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

## (ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..60

(D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp2

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CATTTGCTAG TTTATTCTTG ACATGAAGCG TGCCTAATGG TATATTACTT  
GAGTACTGTT 60

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## (2) INFORMATION FOR SEQ ID NO: 17:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

## (ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp20

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CATGGGTGAG TTTATTCTTG ACAGTGCGGC CNGGGGCTGA TATCATAGCA  
GAGTACTATT 60

## (2) INFORMATION FOR SEQ ID NO: 18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

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## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

## (ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..59

(D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp21

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

CATTACCGAG TTTATTCTTG ACACCGTTTA TCGGGGTTGT ATAATACTAT  
AGTACTGTT 59

## (2) INFORMATION FOR SEQ ID NO: 19:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

## (ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..60

(D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp23

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CATGTAGGAG TTTATTCTTG ACAGATTAGT TAGGGGGTGG TATAATATCT  
CAGTACTGTT 60

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## (2) INFORMATION FOR SEQ ID NO: 20:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

## (ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"
- /label= Cp24

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CATGGGTAAG TTTATTCTTC AACTATCTG GGCCCGATGG TATAATAAGT  
GACTACTGTT 60

## (2) INFORMATION FOR SEQ ID NO: 21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

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cont.

CATTCTACAG TTTATTCTTG ACATTGCACT GTCCCCCTGG TATAATAACT  
ATACATGCAT 60

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

CATGGGGCCG TTTATTCTTG ACAACGGCGA GCAGACCTGG TATAATAATA  
TAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

"Seq ID" 23

Sub  
B1  
Cont

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..59

(D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp29

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CATCGGTAAG TTATTCTTGA CATCTCAGGG GGGACGTGGT ATAATAACTG  
AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..60

(D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp3

6661604592425

Sub  
B  
cont

SEQUENCE DESCRIPTION:  
CTGTAG TTTATTCTTG AC  
ACTGTT 60

FORMATION FOR SEQ ID

SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: YES

ANTI-SENSE: NO

ORIGINAL SOURCE:  
(A) ORGANISM: Lactococcus lactis

FEATURE:  
(A) NAME/KEY: promoter  
(B) LOCATION: 4..60  
(D) OTHER INFORMATION:  
promoter"  
/label= Cp30

SEQUENCE DESCRIPTION:  
ACAGAG TTTATTCTTG AC  
ACTGTT 60

FORMATION FOR SEQ ID

SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(2) INFORMATION FOR SEQ ID NO: 26:

(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(iii) ~~HYPOTHETICAL~~: YES

(vi) ORIGINAL SOURCE:

(ix) **FEATURE:**

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard\_name= "Constitutional promoter"  
/label= Cp30

CATGACAGAG TTTATTCTTG ACAGTATTGG GTTACTTTGG TATAATAGTT  
GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

Sub  
B1  
cont

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..60

(D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp32

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

CATACGGGAG TTTATTCTTG ACATATTGCC GGTGTGTTGG TATAATAACT  
TAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..60

(D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"

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Sub  
B1  
Cont



/label= Cp33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

CATGTTGGAG TTTATTCTTG ACATACAATT ACTGCAGTGA TATAATAGGT  
GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"
- /label= Cp34

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

CATCGCGAAG TTTATTCTTC ACACACCGCA GAACTTGTGG TATAATACAA  
CAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid

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Sub  
B1  
cont

(D) ~~TOPOLOGY~~: linear

(iii) ~~HYPOTHETICAL~~: YES

(vi) ORIGINAL SOURCE:

**(ix) FEATURE:**

(B) LOCATION: 4..59

(D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp37

CATCATTAAG TTTATTCTTC ACATTGGCCG GAATTGTTGT ATAATACCTT  
AGTACTGTT 59

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: nucleic acid

(D) TOPOLOGY: linear

(iii) **HYPOTHETICAL: YES**

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

Sub  
B1  
cont

Label= Cp38

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CATAGAGAAAG TTTATTCTTG ACAGCTAACT TGGCCTTTGA TATAATACAT  
GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) ~~HYPOTHETICAL~~: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Lactococcus lactis*

(ix) **FEATURE:**

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard\_name= "Constitutional promoter"  
/label= Cp39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CATTGCGAAG TTTATTCTTG ACAGTACGTT TTTACCATGA TATAATAGTA  
TAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

Sub  
B1  
cont.

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..60

(D) OTHER INFORMATION: /standard\_name= "Constitutional  
promoter"  
/label= Cp4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

GATGTTTTAG TTTATTCTTG ACACCGTATC GTGCGCGTGA TATAATCGGG  
ATCCTTAAGA 60

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

667777 25927760

Sub  
B1  
Cont.

## (ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4

(D) OTHER INFORMATION:/standard\_name= "Constitutional  
promoter"  
/label= Cp40

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

CATAGAACAG TTTATTCTTG ACATTGAATA AGAAGGCTGA TATAATAGCC  
AGTACTGTT 59

## (2) INFORMATION FOR SEQ ID NO: 35:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

## (ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard\_name= "Constitutional  
promoter"  
/label= Cp41

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

CATCCGCAAG TTTATTCTTG ACAGCTGAAT GTAGACGTGG TATAATAGTT  
AAGTACTGTT 60

## (2) INFORMATION FOR SEQ ID NO: 36:

catcgaacag

Sub  
B1  
Cont

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

## (ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp42

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

CATTCGTAAG TTTATTCTTG ACACCTGAGA TGAGGCGTGA TATAATAAAT  
AAGTACTGTT 60

## (2) INFORMATION FOR SEQ ID NO: 37:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

666722 15924260

*Sub  
B1  
cont*

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..59

(D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp44

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CATCGGGTAG TTTATTCTTG ACAATTAAGT AGAGCCTGAT ATAATAGTTC  
AGTACTGTT 59

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 4..59

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /evidence= EXPERIMENTAL  
/standard\_name= "Constitutional promoter"  
/label= Cp5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CATGGGGGAG TTTATTCTTG ACATCATCTT CGTAGCCTGG TATACTACAT  
GAGTATGTT 59

6611261 2921261

Sub  
B1  
cont

## (2) INFORMATION FOR SEQ ID NO: 39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

## (ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp6

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CATGTGGGAG TTTATTCTTG ACACAGATAT TTCCGGATGA TATAATAACT  
GAGTACTGTT 60

## (2) INFORMATION FOR SEQ ID NO: 40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO



## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

## (ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard\_name= "Constitutional  
promoter"  
/label= Cp7

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

TATGCGGTAG TTTATTCTTG ACATGACGAG ACAGGTGTGG TATAATGGGT  
CTAGATTAGG 60

## (2) INFORMATION FOR SEQ ID NO: 41:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Lactococcus lactis

## (ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION:4..60

(D) OTHER INFORMATION:/standard\_name= "Constitutional  
promoter"  
/label= Cp8

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

CATTCTTTAG TTTATTCTTG ACAAACGTAT TGAGGACTGA TATAATAGGT  
GAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Lactococcus lactis

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 4..60
- (D) OTHER INFORMATION: /standard\_name= "Constitutional promoter"  
/label= Cp9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CATAGTCTAG TTTATTCTTG ACACGCGGTC CATTGGCTGG TATAATAATT  
TAGTACTGTT 60

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

66720-292420

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 8..177

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/standard\_name= "Yeast promoter"

/label= Yp102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GAATTCGTGA CTCAAACGGG TGGTCGACGG GTGGTTCCAA TTAATTGGCG  
TCCCTCTTAT 60

AAAGGCGAGG GTACGTGCGA CAATTGGTAG AGCGAGCGGG GCTCTTAAGT  
GCAAGTGACT 120

GCGAACATTT TTTTCGTTTG TTAGAATAAT TCAAGAATCG CTACCAATCA  
TGGATCC 177

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

66112301 49921260

- (A) NAME/KEY: promoter
- (B) LOCATION:8..181
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/evidence= EXPERIMENTAL  
/standard\_name= "Yeast promoter"  
/label= Yp112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GAATTCGTGA CTCACGGCAT CTGATGGTTG ACCATAGTCA GGAACATTGT  
GCTGGAGTTC 60

CTTGAGGAAT GAGTTATAAA ATGGGAGGTT GCGGCTAATG CCAGGCAGGA  
GAGGAACCCT 120

CTTAAGTGCA AGTGACTGCA AACATTTTTT TCGTTTGTTG AATCGCTACC  
AATCATGGAT 180

CC 182

(2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION:8..181
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION:/evidence= EXPERIMENTAL  
/standard\_name= "Yeast promoter"  
/label= Yp13

66720-254260

ATCATGGATC C 191

(2) INFORMATION FOR SEQ ID NO: 46:

**(i) SEQUENCE CHARACTERISTICS:**

(A) LENGTH: 167 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

**(ix) FEATURE:**

(A) NAME/KEY: promoter

(B) LOCATION:8..167

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: evidence= EXPERIMENTAL

```
/standard name= "Yeast promoter"
```

Label= Yp15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

GAATTCGTGA CTCAGGGCCG TACTAAGTAG CTTTCGTATG CTATGCGGGG  
TTTTATAAAT 60

(A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(B) LOCATION:8..191

(D) OTHER INFORMATION:/evidence= EXPERIMENTAL

```
/standard_name= "Yeast promoter"
```

/label= Yp154

GAATTCGTGA CTCACCGCTC GGGTGCAGGG CCAAGGCGGC GGAATGTGCG  
GGGCGTTCTA 60

CGCGAATCGG GGTATAAATT TATAAGGAGG CTGCGGGTGC TAGTTTGTCT  
AGTTTGACTC 120

TTAAGTGCAA GTGACTGCGA ACATTTTTCG TTTGTTAGAA TAATTCAAGA  
ATCGCTACCA 180

191

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 8..179

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /evidence= EXPERIMENTAL  
/standard\_name= "Yeast promoter"  
/label= Yp183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

GAATTCGTGA CTCACTAAGG GTTCGCCATT AACAGAATCG CTGGTAGAAC  
ATCGGTAGTT 60

AGGCACCCGA GTATAAACAG GCGGACCCCT CACGGATATC AGCTGATAGT  
GCGAGCCTCA 120

ATGCGAACAT TTTTTTCGTT TGTTAGAATA ATTCAAGAAT CGCTACCAAT  
CATGGATCC 179

(2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

661722 49924260



## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

## (ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 8..190

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/standard\_name= "Yest promoter"

/label= Yp190

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

GAATTCGTGA CTCAGTATCC ACGGGTGTTT GAGGGCTGGT CGCAGGTTAG  
CAGGCGAGGG 60

CGGGTGGTTA CGGCTATAAA TGAGTGTTTG CAGCCGGGTA CGGGCGTACG  
AGTAGTGATC 120

TCTTAAATGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC  
AAGAATCGCT 180

ACCAATCATG GATCC

195

## (2) INFORMATION FOR SEQ ID NO: 51:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

## (ix) FEATURE:

(A) NAME/KEY: promoter

/label= Yp191

193

/label= Yp192

TCTTAATTGT TAGAATAATT CAAGAATCGC TACCAATCAT GGATCC  
166

(2) INFORMATION FOR SEQ ID NO: 53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) **HYPOTHETICAL: YES**

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

**(A) ORGANISM: *Saccharomyces cerevisiae***

(ix) **FEATURE:**

(A) NAME/KEY: promoter

(B) LOCATION:8..190

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION:/evidence= EXPERIMENTAL

```
/standard_name= "Yeast promoter"
```

/label= Yp212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GAATTCGTGA CTCAGTCGCC CGCAAGATGG GATGGTG CAT TTTAAACACC  
CGAATTATAC 60

TCGTCAACTT ATAGTATAAA CGGAACGCGA CGATACGTTC TAGTTTTTCGG  
CGAAGTCGAC 120

TCTTAAGTGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC  
AAGAATCGCT 180

ACCAATCATG GATCC

195

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..183
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL  
/standard\_name= "Yeast promoter"  
/label= Yp24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

GAATTCGTAC TCACGACAGC GTTATGACTT CGAGGACCAG CTACTTCCGG  
TCGCGTACTA 60

GTTTTTACCT GTATAAACTT TGCTACCGCT GGGCCTTGGT GGTGCTGTCC  
CGCTCTTAAG 120

TGCAAGTGAC TGCGAACATT TTTTTCGTTT GTTACAATAA TTCAAGAATC  
GCTACCAATC 180

ATGGATCC

188

66120-294420

## (2) INFORMATION FOR SEQ ID NO: 55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

## (iii) HYPOTHETICAL: YES

## (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

## (ix) FEATURE:

- (A) NAME/KEY: promoter
- (B) LOCATION: 8..190
- (C) IDENTIFICATION METHOD: experimental
- (D) OTHER INFORMATION: /evidence= EXPERIMENTAL  
/standard\_name= "Yeast promoter"  
/label= Yp435

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

GAATTCGTGA CTAAATGGAT AAGGTTATCG CCATCACGGA GTCTTCTCTC  
ACGTCTGGAG 60

CAGAGGCTAG ACCTTATAAA TTATACATGG TGGGAGAGGC GATAGTCTTT  
AGAGACGTGC 120

TCTTAAGTGC AAGTGACTGC GAACATTTTT TTCGTTTGTT AGAATAATTC  
AAGAATCGCT 180

ACCAATCATG GATCC

195

## (2) INFORMATION FOR SEQ ID NO: 56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 8..184

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/standard\_name= "Yeast promoter"

/label= Yp68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

GAATTCGTGA CTCACAAGAA TGTGGGCGGG TCGTTAACT GAGCCTGGAC  
ACCTTGGCTG 60

CGTCGCTTTC GTATAAAGAT CTTAGAGCTG TGGAGTCTGG GTCGAGTGGC  
CAGCTCTTAA 120

ATGCAAGTGA CTGCGAACAT TTTTTCGTT TGTTAGAATA ATTCAAGAAT  
CGCTACCAAT 180

CATGGATCC

189

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

(A) NAME/KEY: promoter

(B) LOCATION: 8..190

(C) IDENTIFICATION METHOD: experimental

(D) OTHER INFORMATION: /evidence= EXPERIMENTAL

/standard\_name= "Yeast promoter"

/label= Yp89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GAATTCGTGA CTCACTCGGA AGATTGGGTT TACGATTAGG ATGGCGCGGC  
AGAACCGGGG 60

GGGATTCCCT TCTATATAAA GGGTTCCGAT ACTACGTGCT GCGGACGGCC  
GATCGAGTTA 120

TCTTAAGTGC AAGTGACTGC GAAAATTTTT TTCGTTTGTT AGAATAATTC  
AAGAATCGCT 180

ACCAATCATG GATCC

195

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: YES

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

6667620 19921220

GAATTCGTGA CTCATCTAGT GAGAGGAGCC GTGGTATCTT GTGTCACCAC  
CAGGGGAAAA 60

TAATGGCAGG GGTGTATAAA TGGTCGAGTA GTCGCGACCC ACGCTGCAAG  
GCAAGGAACT 120

CTTAAATTTT TTTCGTTTGT TAGAATAATT CAAGAATCGC TACCAATCAT  
GGATCC 176

Bl  
amt

[illegible]